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RAW SEQUENCE LISTING   DATE: 10/15/2004
PATENT APPLICATION: US/10/645,012   TIME: 10:22:28

Input Set : N:\Crf3\RULE60\10645012.RAW.txt
Output Set: N:\CRF4\10152004\J645012.raw

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 1 <110> APPLICANT: Tsuchiya, Masayuki
 2        Saito, Mikiyoshi
 3        Ohtomo, Toshihiko
 4 <120> TITLE OF INVENTION: NOVEL METHOD FOR GENE CLONING
 5 <130> FILE REFERENCE: 06501-070001
 6 <140> CURRENT APPLICATION NUMBER: 10/645,012
 7 <141> CURRENT FILING DATE: 2003-08-21
 8 <150> PRIOR APPLICATION NUMBER: US/09/700,820
 9 <151> PRIOR FILING DATE: 2000-11-20
10 <150> PRIOR APPLICATION NUMBER: PCT/JP99/02341
11 <151> PRIOR FILING DATE: 1999-04-30
12 <150> PRIOR APPLICATION NUMBER: JP 10/138652
13 <151> PRIOR FILING DATE: 1998-05-20
14 <150> PRIOR APPLICATION NUMBER: JP 10/279876
15 <151> PRIOR FILING DATE: 1998-10-01
16 <160> NUMBER OF SEQ ID NOS: 39
18 <210> SEQ ID NO: 1
19 <211> LENGTH: 15
20 <212> TYPE: PRT
21 <213> ORGANISM: Artificial Sequence
22 <220> FEATURE:
23 <223> OTHER INFORMATION: Description of Artificial Sequence:Peptide Linker Sequence
24 <400> SEQUENCE: 1
25        Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser
26         1               5                  10                  15
28 <210> SEQ ID NO: 2
29 <211> LENGTH: 1035
30 <212> TYPE: DNA
31 <213> ORGANISM: Homo sapiens
32 <220> FEATURE:
33 <221> NAME/KEY: CDS
34 <222> LOCATION: (1)..(1035)
35 <400> SEQUENCE: 2
36        atg ctg gcc gtc ggc tgc gcg ctg ctg gct gcc ctg ctg gcc gcg ccg      48
37        Met Leu Ala Val Gly Cys Ala Leu Leu Ala Ala Leu Leu Ala Ala Pro
38         1               5                  10                  15
39        gga gcg gcg ctg gcc cca agg cgc tgc cct gcg cag gag gtg gca aga      96
40        Gly Ala Ala Leu Ala Pro Arg Arg Cys Pro Ala Gln Glu Val Ala Arg
41                       20                  25                  30
42        ggc gtg ctg acc agt ctg cca gga gac agc gtg act ctg acc tgc ccg     144
43        Gly Val Leu Thr Ser Leu Pro Gly Asp Ser Val Thr Leu Thr Cys Pro
44                       35                  40                  45
45        ggg gta gag ccg gaa gac aat gcc act gtt cac tgg gtg ctc agg aag     192
```

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46    Gly Val Glu Pro Glu Asp Asn Ala Thr Val His Trp Val Leu Arg Lys
47        50                  55                  60
48    ccg gct gca ggc tcc cac ccc agc aga tgg gct ggc atg gga agg agg    240
49    Pro Ala Ala Gly Ser His Pro Ser Arg Trp Ala Gly Met Gly Arg Arg
50    65                  70                  75                  80
51    ctg ctg ctg agg tcg gtg cag ctc cac gac tct gga aac tat tca tgc    288
52    Leu Leu Leu Arg Ser Val Gln Leu His Asp Ser Gly Asn Tyr Ser Cys
53                        85                  90                  95
54    tac cgg gcc ggc cgc cca gct ggg act gtg cac ttg ctg gtg gat gtt    336
55    Tyr Arg Ala Gly Arg Pro Ala Gly Thr Val His Leu Leu Val Asp Val
56                        100                 105                 110
57    ccc ccc gag gag ccc cag ctc tcc tgc ttc cgg aag agc ccc ctc agc    384
58    Pro Pro Glu Glu Pro Gln Leu Ser Cys Phe Arg Lys Ser Pro Leu Ser
59                    115                 120                 125
60    aat gtt gtt tgt gag tgg ggt cct cgg agc acc cca tcc ctg acg aca    432
61    Asn Val Val Cys Glu Trp Gly Pro Arg Ser Thr Pro Ser Leu Thr Thr
62            130                 135                 140
63    aag gct gtg ctc ttg gtg agg aag ttt cag aac agt ccg gcc gaa gac    480
64    Lys Ala Val Leu Leu Val Arg Lys Phe Gln Asn Ser Pro Ala Glu Asp
65    145                 150                 155                 160
66    ttc cag gag ccg tgc cag tat tcc cag gag tcc cag aag ttc tcc tgc    528
67    Phe Gln Glu Pro Cys Gln Tyr Ser Gln Glu Ser Gln Lys Phe Ser Cys
68                        165                 170                 175
69    cag tta gca gtc ccg gag gga gac agc tct ttc tac ata gtg tcc atg    576
70    Gln Leu Ala Val Pro Glu Gly Asp Ser Ser Phe Tyr Ile Val Ser Met
71                        180                 185                 190
72    tgc gtc gcc agt agt gtc ggg agc aag ttc agc aaa act caa acc ttt    624
73    Cys Val Ala Ser Ser Val Gly Ser Lys Phe Ser Lys Thr Gln Thr Phe
74                        195                 200                 205
75    cag ggt tgt gga atc ttg cag cct gat ccg cct gcc aac atc aca gtc    672
76    Gln Gly Cys Gly Ile Leu Gln Pro Asp Pro Pro Ala Asn Ile Thr Val
77                    210                 215                 220
78    act gcc gtg gcc aga aac ccc cgc tgg ctc agt gtc acc tgg caa gac    720
79    Thr Ala Val Ala Arg Asn Pro Arg Trp Leu Ser Val Thr Trp Gln Asp
80    225                 230                 235                 240
81    ccc cac tcc tgg aac tca tct ttc tac aga cta cgg ttt gag ctc aga    768
82    Pro His Ser Trp Asn Ser Ser Phe Tyr Arg Leu Arg Phe Glu Leu Arg
83                    245                 250                 255
84    tat cgg gct gaa cgg tca aag aca ttc aca aca tgg atg gtc aag gac    816
85    Tyr Arg Ala Glu Arg Ser Lys Thr Phe Thr Thr Trp Met Val Lys Asp
86                    260                 265                 270
87    ctc cag cat cac tgt gtc atc cac gac gcc tgg agc ggc ctg agg cac    864
88    Leu Gln His His Cys Val Ile His Asp Ala Trp Ser Gly Leu Arg His
89                    275                 280                 285
90    gtg gtg cag ctt cgt gcc cag gag gag ttc ggg caa ggc gag tgg agc    912
91    Val Val Gln Leu Arg Ala Gln Glu Glu Phe Gly Gln Gly Glu Trp Ser
92            290                 295                 300
93    gag tgg agc ccg gag gcc atg ggc acg cct tgg aca gaa tcc agg agt    960
94    Glu Trp Ser Pro Glu Ala Met Gly Thr Pro Trp Thr Glu Ser Arg Ser
```

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```
 95        305                310              315              320
 96        cct cca gct gag aac gag gtg tcc acc ccc atg cag gca ctt act act      1008
 97        Pro Pro Ala Glu Asn Glu Val Ser Thr Pro Met Gln Ala Leu Thr Thr
 98                           325              330              335
 99        aat aaa gac gat gat aat att ctc ttc                                  1035
100         Asn Lys Asp Asp Asp Asn Ile Leu Phe
101                    340              345
103 <210> SEQ ID NO: 3
104 <211> LENGTH: 40
105 <212> TYPE: DNA
106 <213> ORGANISM: Artificial Sequence
107 <220> FEATURE:
108 <223> OTHER INFORMATION: Description of Artificial Sequence: "IL6R1", an artificially
synthesized primer sequence
109 <400> SEQUENCE: 3
110        ttcgaattcc caccatgctg gccgtcggct gcgcgctgct                         40
112 <210> SEQ ID NO: 4
113 <211> LENGTH: 36
114 <212> TYPE: DNA
115 <213> ORGANISM: Artificial Sequence
116 <220> FEATURE:
117 <223> OTHER INFORMATION: Description of Artificial Sequence: "IL6R2", an artificially
synthesized primer sequence
118 <400> SEQUENCE: 4
119        ttcgaattcg aagagaatat tatcatcgtc tttatt                             36
121 <210> SEQ ID NO: 5
122 <211> LENGTH: 768
123 <212> TYPE: DNA
124 <213> ORGANISM: Artificial Sequence
125 <220> FEATURE:
126 <221> NAME/KEY: CDS
127 <222> LOCATION: (1)..(768)
128 <220> FEATURE:
129 <223> OTHER INFORMATION: Description of Artificial Sequence: a designed single chain
Fv gene sequence
130 <400> SEQUENCE: 5
131        cag gtc caa ctg cag gag agc ggt cca ggt ctt gtg aga cct agc cag      48
132        Gln Val Gln Leu Gln Glu Ser Gly Pro Gly Leu Val Arg Pro Ser Gln
133        1               5                   10               15
134        acc ctg agc ctg acc tgc acc gtg tct ggc tac tca att acc agc gat      96
135        Thr Leu Ser Leu Thr Cys Thr Val Ser Gly Tyr Ser Ile Thr Ser Asp
136                         20                  25               30
137        cat gcc tgg agc tgg gtt cgc cag cca cct gga cga ggt ctt gag tgg     144
138        His Ala Trp Ser Trp Val Arg Gln Pro Pro Gly Arg Gly Leu Glu Trp
139                    35                  40                  45
140        att gga tac att agt tat agt gga atc aca acc tat aat cca tct ctc     192
141        Ile Gly Tyr Ile Ser Tyr Ser Gly Ile Thr Thr Tyr Asn Pro Ser Leu
142             50                  55                  60
143        aaa tcc aga gtg aca atg ctg aga gac acc agc aag aac cag ttc agc     240
144        Lys Ser Arg Val Thr Met Leu Arg Asp Thr Ser Lys Asn Gln Phe Ser
145        65                  70                  75                  80
146        ctg aga ctc agc agc gtg aca gcc gcc gac acc gcg gtt tat tat tgt     288
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Output Set: **N:\CRF4\10152004\J645012.raw**

147	Leu Arg Leu Ser Ser Val Thr Ala Ala Asp Thr Ala Val Tyr Tyr Cys	
148	85 90 95	
149	gca aga tcc cta gct cgg act acg gct atg gac tac tgg ggt caa ggc	336
150	Ala Arg Ser Leu Ala Arg Thr Thr Ala Met Asp Tyr Trp Gly Gln Gly	
151	100 105 110	
152	agc ctc gtc aca gtc tcc tca ggt ggt ggt ggt tcg ggt ggt ggt ggt	384
153	Ser Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly	
154	115 120 125	
155	tcg ggt ggt ggc gga tcg gac atc cag atg acc cag agc cca agc agc	432
156	Ser Gly Gly Gly Gly Ser Asp Ile Gln Met Thr Gln Ser Pro Ser Ser	
157	130 135 140	
158	ctg agc gcc agc gtg ggt gac aga gtg acc atc acc tgt aga gcc agc	480
159	Leu Ser Ala Ser Val Gly Asp Arg Val Thr Ile Thr Cys Arg Ala Ser	
160	145 150 155 160	
161	cag gac atc agc agt tac ctg aat tgg tac cag cag aag cca gga aag	528
162	Gln Asp Ile Ser Ser Tyr Leu Asn Trp Tyr Gln Gln Lys Pro Gly Lys	
163	165 170 175	
164	gct cca aag ctg ctg atc tac tac acc tcc aga ctg cac tct ggt gtg	576
165	Ala Pro Lys Leu Leu Ile Tyr Tyr Thr Ser Arg Leu His Ser Gly Val	
166	180 185 190	
167	cca agc aga ttc agc ggt agc ggt agc ggt acc gac ttc acc ttc acc	624
168	Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Phe Thr	
169	195 200 205	
170	atc agc agc ctc cag cca gag gac atc gct acc tac tac tgc caa cag	672
171	Ile Ser Ser Leu Gln Pro Glu Asp Ile Ala Thr Tyr Tyr Cys Gln Gln	
172	210 215 220	
173	ggt aac acg ctt cca tac acg ttc ggc caa ggg acc aag gtg gaa atc	720
174	Gly Asn Thr Leu Pro Tyr Thr Phe Gly Gln Gly Thr Lys Val Glu Ile	
175	225 230 235 240	
176	aaa cga act gtg gct gca cca tct gtc ttc atc ttc ccg cca tct gat	768
177	Lys Arg Thr Val Ala Ala Pro Ser Val Phe Ile Phe Pro Pro Ser Asp	
178	245 250 255	

180 <210> SEQ ID NO: 6
181 <211> LENGTH: 32
182 <212> TYPE: DNA
183 <213> ORGANISM: Artificial Sequence
184 <220> FEATURE:
185 <223> OTHER INFORMATION: Description of Artificial Sequence: "TMT1", an artificially
synthesized primer sequence
186 <400> SEQUENCE: 6
187 ggtgtcgact cccaggtcca actgcaggag ag   32
189 <210> SEQ ID NO: 7
190 <211> LENGTH: 32
191 <212> TYPE: DNA
192 <213> ORGANISM: Artificial Sequence
193 <220> FEATURE:
194 <223> OTHER INFORMATION: Description of Artificial Sequence: "LINK1", an artificially
synthesized primer sequence
195 <400> SEQUENCE: 7
196 ctcgtcacag tctcctcagg tggtggtggt tc   32
198 <210> SEQ ID NO: 8

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199 <211> LENGTH: 38
200 <212> TYPE: DNA
201 <213> ORGANISM: Artificial Sequence
202 <220> FEATURE:
203 <223> OTHER INFORMATION: Description of Artificial Sequence: "LINK3", an artificially
synthesized primer sequence
204 <400> SEQUENCE: 8
205   gacatccaga tgacccagag cccaagcagc ctgagcgc   38
207 <210> SEQ ID NO: 9
208 <211> LENGTH: 63
209 <212> TYPE: DNA
210 <213> ORGANISM: Artificial Sequence
211 <220> FEATURE:
212 <223> OTHER INFORMATION: Description of Artificial Sequence: "SCP-C", an artificially
synthesized primer sequence
213 <400> SEQUENCE: 9
214   gctgaattct tattatttat cgtcatcgtc tttgtagtca agcttatcag atggcgggaa   60
215   gat   63
217 <210> SEQ ID NO: 10
218 <211> LENGTH: 9
219 <212> TYPE: PRT
220 <213> ORGANISM: Artificial Sequence
221 <220> FEATURE:
222 <223> OTHER INFORMATION: Description of Artificial Sequence: FLAG peptide
223 <400> SEQUENCE: 10
224   Met Asp Tyr Lys Asp Asp Asp Asp Lys
225   1   5
227 <210> SEQ ID NO: 11
228 <211> LENGTH: 34
229 <212> TYPE: DNA
230 <213> ORGANISM: Artificial Sequence
231 <220> FEATURE:
232 <223> OTHER INFORMATION: Description of Artificial Sequence: "LINK2", an artificially
synthesized primer sequence
233 <400> SEQUENCE: 11
234   aaccaccacc acctgaggag actgtgacga ggct   34
236 <210> SEQ ID NO: 12
237 <211> LENGTH: 35
238 <212> TYPE: DNA
239 <213> ORGANISM: Artificial Sequence
240 <220> FEATURE:
241 <223> OTHER INFORMATION: Description of Artificial Sequence: "LINK4", an artificially
synthesized primer sequence
242 <400> SEQUENCE: 12
243   aggctgcttg ggctctgggt catctggatg tccga   35
245 <210> SEQ ID NO: 13
246 <211> LENGTH: 36
247 <212> TYPE: DNA
248 <213> ORGANISM: Artificial Sequence
249 <220> FEATURE:
250 <223> OTHER INFORMATION: Description of Artificial Sequence: "TMT2", an artificially
synthesized primer sequence
251 <400> SEQUENCE: 13

252   atccgcggcc gcttattatt tatcgtcatc gtcttt   36

RAW SEQUENCE LISTING ERROR SUMMARY   DATE: 10/15/2004
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Input Set : **N:\Crf3\RULE60\10645012.RAW.txt**
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Invalid Line Length:
The rules require that a line not exceed 72 characters in length. This includes spaces.

Seq#:1; Line(s) 23
Seq#:3; Line(s) 108
Seq#:4; Line(s) 117
Seq#:5; Line(s) 129
Seq#:6; Line(s) 185
Seq#:7; Line(s) 194
Seq#:8; Line(s) 203
Seq#:9; Line(s) 212
Seq#:11; Line(s) 232
Seq#:12; Line(s) 241
Seq#:13; Line(s) 250
Seq#:15; Line(s) 270
Seq#:16; Line(s) 280
Seq#:18; Line(s) 477
Seq#:19; Line(s) 486
Seq#:20; Line(s) 495
Seq#:21; Line(s) 507
Seq#:22; Line(s) 620
Seq#:23; Line(s) 633
Seq#:26; Line(s) 758
Seq#:27; Line(s) 838
Seq#:28; Line(s) 918
Seq#:29; Line(s) 927
Seq#:30; Line(s) 940
Seq#:31; Line(s) 1047
Seq#:32; Line(s) 1056
Seq#:33; Line(s) 1065
Seq#:34; Line(s) 1077
Seq#:35; Line(s) 1205
Seq#:36; Line(s) 1214
Seq#:37; Line(s) 1224
Seq#:38; Line(s) 1233
Seq#:39; Line(s) 1245

VERIFICATION SUMMARY
PATENT APPLICATION: US/10/645,012

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L:295 M:351 W: Sequence data Name/Key Feature Out-of-Range, SEQ ID#: 17, CDS LOCATION:29..2839